



**Fig. S6. RNaseq analysis and differentiation potential of *Lin28a*-overexpressing MuSCs.**

(a) Volcano plot analysis for genes that are differentially expressed in conventional MuSCs overexpressing *Lin28a*, relative to conventional MuSCs.

(b) Signatures enriched in con MuSCs overexpressing *Lin28a* (black) or empty vector (white), as identified by Gene Set Enrichment Analysis.

(c) Representative GSEA profiles with normalized enrichment scores (NES) and nominal P values are shown.

(d) Quantitative RT-PCR for adipogenesis, osteogenesis and vascular genes' expression in Lin28a-tDTo+ MuSCs overexpressing *Lin28a* relative to the empty vector (CTRL). Data are mean  $\pm$  SEM. N = 3 independent experiments.

\* P < 0.05, \*\* P < 0.01, \*\*\* P < 0.001.

(e) Quantitative RT-PCR and Western blot analyses for *Lin28a* expression (Lin28a-T2A (32 kD)) in con or Lin28a+ MuSCs overexpressing *Lin28a* or empty vector by retrovirus.